CLAIMS

What is claimed is:

subA2

1. A method for identifying relative binding motifs of peptide-like molecules, comprising the steps of:

(a) training an artificial neural network (ANN) with a set of training peptide-like molecules, each of known sequence and binding affinity;

(b) applying to the ANN at least one peptide-like molecule, each of known sequence but unknown binding affinity;

(c) analyzing each applied test peptide-like molecule using the ANN to predict a relative binding affinity for each test peptide-like molecule.

2. A method for identifying relative peptide binding motifs, comprising the steps of:

(a) training an artificial neural network (ANN) with a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(b) applying to the ANN at least one peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(c) analyzing each applied test peptide using the ANN to predict a relative binding affinity for each test peptide.

3. The method of claim 2, wherein the set of training peptides include peptides having a binding affinity for MHC class I molecules.

4. The method of claim 3, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

5. The method of claim 2, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

6. The method of claim 5, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

7. The method of claims 1 or 2, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

8. A system for identifying relative binding motifs for peptide-like molecules, comprising:

(a) means for training an artificial neural network (ANN) with a set of training peptide-like molecules, each of known sequence and binding affinity;

(b) means for applying to the ANN at least one test peptide-like molecule, each of known sequence but unknown binding affinity;

(c) means for analyzing each applied test peptide-like molecule using the ANN to predict a relative binding affinity for each test peptide-like molecule.

9. A system for identifying relative peptide binding motifs, comprising:

(a) means for training an artificial neural network (ANN) with a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(b) means for applying to the ANN at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(c) means for analyzing each applied test peptide using the ANN to predict a relative binding affinity for each test peptide.

10. The system of claim 9, wherein the set of training peptides include peptides having a binding affinity for MHC class I molecules.

11. The system of claim 10, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

12. The system of claim 9, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

13. The system of claim 12, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

14. The system of claims 8 or 9, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

15. A computer program, residing on a computer-readable medium, for identifying relative binding motifs for peptide-like molecules, comprising instructions for causing a computer to:

(a) train an artificial neural network (ANN) with a set of training peptide-like molecules, each of known sequence and binding affinity;

(b) apply to the ANN at least one test peptide-like molecule, each of known sequence but unknown binding affinity;

(c) analyze each applied test peptide-like molecule using the ANN to predict a relative binding affinity for each test peptide-like molecule.

16. A computer program, residing on a computer-readable medium, for identifying relative peptide binding motifs, comprising instructions for causing a computer to:

(a) train an artificial neural network (ANN) with a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(b) apply to the ANN at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(c) analyze each applied test peptide using the ANN to predict a relative binding affinity for each test peptide.

17. The computer program of claim 16, wherein the set of training peptides having a binding affinity for MHC class I molecules.

18. The computer program of claim 17, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

19. The computer program of claim 16, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

20. The computer program of claim 19, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

21. The computer program of claims 15 or 16, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.